

Transcriptomic profiling does not refine mastocytosis diagnosis

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Supplementary Figure Legends

Supplementary Table 1 (see excel file)

Detailed clinical characteristics of the analyzed cohort for each individual patient.

Supplementary Table 2 (see excel file)

Raw differential expression data for all WHO subtypes vs. healthy and output data for UpSet plots shown in Fig 2B, C and D. Genes differentially expressed between the shown WHO subtypes as well as gene sets enriched highly or lowly between WHO subtypes.

Supplementary Table 3 (see excel file)

Correlation analysis (Pearson and Spearman) of all available laboratory values.

Raw CPM values for all samples sequenced and analyzed in this work (read_counts_all_cpm_filt_TMMnor). This dataset can be used for further research.